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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=1; day=30; hr=15; min=41; sec=49; ms=754;]

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Application No: 10533642

Version No: 1.1

Input Set:

Output Set:

Started: 2008-01-30 15:39:52.219

Finished: 2008-01-30 15:39:53.716

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 497 ms

Total Warnings: 57

Total Errors: 0

No. of SeqIDs Defined: 57

Actual SeqID Count: 57

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| W 213 | Artificial or Unknown found in <213> in SEQ ID (2) |
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| W 213 | Artificial or Unknown found in <213> in SEQ ID (16) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (17) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (18) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (19) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (20) |

Input Set:

Output Set:

Started: 2008-01-30 15:39:52.219
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Total Warnings: 57
Total Errors: 0
No. of SeqIDs Defined: 57
Actual SeqID Count: 57

Error code

Error Description

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SEQUENCE LISTING

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<120> METHOD FOR SCREENING MODULATORS OF MITOCHONDRIAL FUCTIONNING AND
NEW MODULATORS OBTAINED

<130> 60815-2230

<140> 10533642

<141> 2008-01-30

<150> US 60/472,725

<151> 2003-05-23

<150> PCT/EP03/12056

<151> 2003-10-03

<150> US 60/415/092

<151> 2002-10-02

<160> 57

<170> PatentIn version 3.3

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<212> PRT

<213> Artificial sequence

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| Arg | Lys | Lys | Arg | Arg | Gln | Arg | Arg | Arg | Gly | Gly | Ala | Thr | Leu | Ser | Ala |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

| | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
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Arg Lys Lys Arg Arg Gln Arg Arg Arg Cys Gly Gly Leu Glu Thr Arg
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Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys Gln Ile Gln Lys
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Val Glu Thr Trp Ala Leu Arg His
35 40

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1 5 10 15

Lys Gly Ala Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Val Lys
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Thr Glu Ser Trp Ile Leu Arg Asn
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Gly Gly Cys Arg Gly Asp Met Phe Gly Cys Gly Gly Leu Leu Phe Ile
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His Phe Arg Ile Gly Ser Arg His Ser Arg Ile Gly
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Arg Ile Glu Ile Trp Ile Leu Arg His
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Ile Leu Arg His
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Arg Lys Lys Arg Arg Gln Arg Arg Arg Gly Gly Arg Ile Ala Ile Trp
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Ile Leu Arg His
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Glu His Trp Ser Tyr Trp Leu Arg Pro Gly Gly Gly Leu Leu Phe Ile
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His Phe Arg Ile Gly Cys Arg His Ser Arg Ile Gly
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1 5 10 15

Leu Phe Ile His Phe Arg Ile Gly Cys Arg His Ser Arg Ile Gly
20 25 30

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1 5 10 15

Ala Gln Arg Ile Glu Ile Trp Ile Leu Arg His
20 25

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1 5 10 15

Ala Gln Arg Ile Glu Thr Trp Ile Leu Arg His
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Arg Lys Lys Arg Arg Gln Arg Arg Arg Gly Gly Gly Ala Trp Lys His
1 5 10 15

Ala Gln Arg Val Glu Ser Trp Ile Leu Arg Asn
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1 5 10 15

Ala Cys Arg Met Glu Thr Trp Ile Leu Arg His
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1 5 10 15

Ile Gln Lys Val Glu Thr Trp Ala Leu Arg His
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1 5 10 15

Val Glu Lys Val Glu Thr Trp Ala Leu Arg His
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Arg Lys Lys Arg Arg Gln Arg Arg Arg Gly Gly Gly Ala Trp Lys His
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Ala Gln Arg Ile Ala Ile Trp Ile Leu Arg His
20 25

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1 5 10 15

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1 5 10 15

Trp Ile Leu Arg His
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Trp Ile Leu Arg His
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Ile Trp Ile Leu Arg His
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<222> (3)..(11)

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Ile Trp Ile Leu Arg His
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<400> 24

Glu His Trp Ser Tyr Trp Leu Arg Pro Gly Gly Gly Arg Ile Glu Ile
1 5 10 15

Trp Ile Leu Arg His
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<400> 25

Glu His Trp Ser Tyr Trp Leu Arg Pro Gly Gly Gly Arg Ile Ala Ile
1 5 10 15

Trp Ile Leu Arg His
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<400> 26

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1 5 10 15

Ile Glu Ile Trp Ile Leu Arg His
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Glu His Trp Ser Tyr Trp Leu Arg Pro Gly Gly Gly Gly Gly Ser Arg
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Ile Ala Ile Trp Ile Leu Arg His
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<400> 28

Glu His Trp Ser Tyr Trp Leu Arg Pro Gly Gly Gly Gly Gly Ser Gly
1 5 10 15

Ala Trp Lys His Ala Gln Arg Ile Glu Ile Trp Ile Leu Arg His
20 25 30

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Glu His Trp Ser Tyr Trp Leu Arg Pro Gly Gly Gly Gly Gly Ser Gly
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Ala Trp Lys His Ala Gln Arg Ile Ala Ile Trp Ile Leu Arg His
20 25 30

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Glu His Trp Ser Tyr Trp Leu Arg Pro Gly Gly Gly Leu Leu Phe Ile
1 5 10 15

His Phe Lys Ile Gly Cys Lys His Ser Lys Ile Gly
20 25

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Glu His Trp Ser Tyr Trp Leu Arg Pro Gly Gly Gly Gly Gly Ser Leu
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Leu Phe Ile His Phe Lys Ile Gly Cys Lys His Ser Lys Ile Gly
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His Phe Arg Ile Gly Ser Arg His Ser Arg Ile Gly
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1 5 10 15

Leu Phe Ile His Phe Arg Ile Gly Ser Arg His Ser Arg Ile Gly
20 25 30

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1 5 10 15

His Phe Lys Ile Gly Ser Lys His Ser Lys Ile Gly
20 25

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<400> 35

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Leu Phe Ile His Phe Lys Ile Gly Ser Lys His Ser Lys Ile Gly
20 25 30

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<400> 36

Arg Lys Lys Arg Arg Gln Arg Arg Arg Gly Gly Gly Ala Trp Lys His
1 5 10 15

Ala Gln Arg Ile Glu Ile Trp Ile Leu Arg His
20 25

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<400> 37

Arg Lys Lys Arg Arg Gln Arg Arg Arg Gly Gly Gly Ala Trp Lys His
1 5 10 15

Ala Gln Arg Ile Glu Thr Trp Ile Leu Arg His
20 25

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<400> 38

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1 5 10 15

Ala Gln Arg Val Glu Ser Trp Ile Leu Arg Asn
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1 5 10 15

Ala Cys Arg Met Glu Thr Trp Ile Leu Arg His

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Ile Gln Lys Val Glu Thr Trp Ala Leu Arg His
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<400> 41

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 1 5 10 15

Val Glu Lys Val Glu Thr Trp Ala Leu Arg His
 20 25

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<400> 42

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Trp Ile Leu Arg His
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<400> 43

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Trp Ile Leu Arg His
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Ile Glu Ile Trp Ile Leu Arg His
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Glu His Trp Ser Tyr Trp Leu Arg Pro Gly Gly Gly Gly Gly Ser Arg
1 5 10 15

Ile Ala Ile Trp Ile Leu Arg His
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Glu His Trp Ser Tyr Trp Leu Arg Pro Gly Gly Gly Gly Gly Ser Gly
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Ala Trp Lys His Ala Gln Arg Ile Glu Ile Trp Ile Leu Arg His
20 25 30

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Glu His Trp Ser Tyr Trp Leu Arg Pro Gly Gly Gly Gly Gly Ser Gly
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Ala Trp Lys His Ala Gln Arg Ile Ala Ile Trp Ile Leu Arg His
20 25 30

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Glu His Trp Ser Tyr Trp Leu Arg Pro Gly Gly Gly Leu Leu Phe Ile
1 5 10 15

His Phe Lys Ile Gly Cys Lys His Ser Lys Ile Gly
20 25

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Glu His Trp Ser Tyr Trp Leu Arg Pro Gly Gly Gly Gly Gly Ser Leu
1 5 10 15

Leu Phe Ile His Phe Lys Ile Gly Cys Lys His Ser Lys Ile Gly
20 25 30

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1 5 10 15

His Phe Arg Ile Gly Ser Arg His Ser Arg Ile Gly
20 25

<210> 51

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1 5 10 15

Leu Phe Ile His Phe Arg Ile Gly Ser Arg His Ser Arg Ile Gly
20 25 30

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<211> 28

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